

SEQUENCE LISTING

<110> EISAI CO., LTD.

<120> Screening method

<130> E1-A0410Y1P

<150> JP 2004-31591

<151> 2004-02-09

<150> JP 2004-368509

<151> 2004-12-20

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(429)

<223>

<400> 1

atg gcc agg tac atg ctg ctg ctg ctc ctg gcg gta tgg gtg ctg acc	48
Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr	
1 5 10 15	

ggg gag ctg tgg ccg gga gct gag gcc cgg gca gcg cct tac ggg gtc	96
Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val	
20 25 30	

agg ctt tgc ggc cga gaa ttc atc cga gca gtc atc ttc acc tgc ggg	144
Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly	
35 40 45	

ggc tcc cgg tgg aga cga tca gac atc ctg gcc cac gag gct atg gga	192
Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly	
50 55 60	

gat acc ttc ccg gat gca gat gct gat gaa gac agt ctg gca ggc gag	240
Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu	

65	70	75	80	
ctg gat gag gcc atg ggg tcc agc gag tgg ctg gcc ctg acc aag tca				288
Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser				
85		90	95	
ccc cag gcc ttt tac agg ggg cga ccc agc tgg caa gga acc cct ggg				336
Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly				
100	105		110	
gtt ctt cgg ggc agc cga gat gtc ctg gct ggc ctt tcc agc agc tgc				384
Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys				
115	120		125	
tgc aag tgg ggg tgt agc aaa agt gaa atc agt agc ctt tgc tag				429
Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys				
130	135		140	

<210> 2
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr
1 5 10 15

Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
20 25 30

Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
35 40 45

Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
50 55 60

Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu
65 70 75 80

Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser
85 90 95

Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly
 100 105 110

Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys
 115 120 125

Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
 130 135 140

<210> 3
 <211> 1857
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (361).. (1770)
 <223>

<400> 3
 gatttgggga gttatgcgcc agtgcgccag tgaccgcggg acacggagag gggaagtctg 60
 cgttgtacat aaggacctag ggactccgag cttggcctga gaacccttgg acgccgagtg 120
 ctctgccttac gggctgcact cctcaactct gctccaaagc agccgctgag ctcaactcct 180
 gcgtccaggg cgctcgtgc gcgccaggac gcgcttagta cccagttcct gggctctctc 240
 ttcagtagct gctttgaaag ctcccacgca cgtcccgag gctagcctgg caacaaaact 300
 ggggtaaacc gtgttatctt aggtcttgtc cccagaaca tgacctagag gtacctgcgc 360
 atg cag atg gcc gat gca gcc acg ata gcc acc atg aat aag gca gca 408
 Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
 1 5 10 15
 ggc ggg gac aag cta gca gaa ctc ttc agt ctg gtc ccg gac ctt ctg 456
 Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
 20 25 30
 gag gcg gcc aac acg agt ggt aac gcg tcg ctg cag ctt ccg gac ttg 504
 Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
 35 40 45

gtg atg ggc gag gag ctg tgc ctg gtg cgt ttc ccg gac aag ttg ctg	1128
Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu	
245 250 255	
ggc cgc gac agg cag ttc tgg ctg ggc ctc tac cac tcg cag aag gtg	1176
Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val	
260 265 270	
ctg ttg ggc ttc gtg ctg ccg ctg ggc atc att atc ttg tgc tac ctg	1224
Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu	
275 280 285	
ctg ctg gtg cgc ttc atc gcc gac cgc cgc gcg gcg ggg acc aaa gga	1272
Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly	
290 295 300	
ggg gcc gcg gta gcc gga gga cgc ccg acc gga gcc agc gcc cgg aga	1320
Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg	
305 310 315 320	
ctg tcg aag gtc acc aaa tca gtg acc atc gtt gtc ctg tcc ttc ttc	1368
Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe	
325 330 335	
ctg tgt tgg ctg ccc aac cag gcg ctc acc acc tgg agc atc ctc atc	1416
Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile	
340 345 350	
aag ttc aac gcg gtg ccc ttc agc cag gag tat ttc ctg tgc cag gta	1464
Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val	
355 360 365	
tac gcg ttc cct gtg agc gtg tgc cta gcg cac tcc aac agc tgc ctc	1512
Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu	
370 375 380	
aac ccc gtc ctc tac tgc ctc gtg cgc cgc gag ttc cgc aag gcg ctc	1560
Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu	
385 390 395 400	
aag agc ctg ctg tgg cgc atc gcg tct cct tcg atc acc agc atg cgc	1608
Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg	
405 410 415	
ccc ttc acc gcc act acc aag ccg gag cac gag gat cag ggg ctg cag	1656
Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln	
420 425 430	

gcc ccg gcg ccg ccc cac gcg gcc gcg gag ccg gac ctg ctc tac tac 1704
 Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
 435 440 445

cca cct ggc gtc gtg gtc tac agc ggg ggg cgc tac gac ctg ctg ccc 1752
 Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
 450 455 460

agc agc tct gcc tac tga cgcaggcctc aggccaggg cgcgccgtcg 1800
 Ser Ser Ser Ala Tyr
 465

gggcaagggtg gccttccccg ggcggtaaag aggtgaaagg atgaaggagg gctgggg 1857

<210> 4
 <211> 469
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
 1 5 10 15

Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
 20 25 30

Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
 35 40 45

Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His
 50 55 60

Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val
 65 70 75 80

Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu
 85 90 95

Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp

100

105

110

Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp
 115 120 125

Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu
 130 135 140

Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met
 145 150 155 160

Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met
 165 170 175

Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg
 180 185 190

Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp
 195 200 205

Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu
 210 215 220

Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys
 225 230 235 240

Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu
 245 250 255

Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val
 260 265 270

Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu
 275 280 285

Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly

290

295

300

Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
 305 310 315 320

Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
 325 330 335

Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
 340 345 350

Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
 355 360 365

Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
 370 375 380

Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
 385 390 395 400

Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
 405 410 415

Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln
 420 425 430

Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
 435 440 445

Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
 450 455 460

Ser Ser Ser Ala Tyr
 465

<210> 5

<211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A sense primer

<400> 5
 gatatcgccg ccaccatgca gatggccgat gcagccac 38

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> An antisense primer

<400> 6
 gatattctcag taggcagagc tgctgggc 28

<210> 7
 <211> 5020
 <212> DNA
 <213> Plasmid

<400> 7
 ctgcagcctg aatatgggcc aaacaggata tctgtggtaa gcagttcctg ccccggtca 60
 gggccaagaa cagatggaac agctgaatat gggccaaaca ggatatctgt ggtaagcagt 120
 tcctgccccg gtcaggggcc aagaacagat ggtccccaga tgcggtccag ccctcagcag 180
 tttctagaga accatcagat gtttcagggt tgccccaagg acctgaaatg accctgtgcc 240
 ttatttgaac taaccaatca gttcgcttct cgcttctgtt cgcgcgcttc tgctccccga 300
 gctcaataaa agagcccaca accctcact cggggcgcca gtcttcgat tgactgagtc 360
 gcccggttac ccgtgtatcc aataaacctt cttgcagttg catccgactt gtggtctogc 420
 tgttccttgg gaggtctcc tctgagtgat tgactaccgc tcagcggggg tctttcattt 480
 gggggctcgt ccgggatcgg gagaccctg cccagggacc accgaccac caccgggagg 540
 taagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta 600

tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcggacc cgtggtggaa	660
ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccagggac ttgggggcc	720
gtttttgtgg cccgacctga ggaagggagt cgatgtggaa tccgaccccg tcaggatatg	780
tggttctggt aggagacgag aacctaaaac agttcccgc tccgtctgaa tttttgcitt	840
cggtttggaa ccgaagccgc gcgtcttgtc tgcgcagca tcgttctgtg ttgtctctgt	900
ctgactgtgt ttctgtatit gtctgaaaat tagggccaga ctgttaccac tcccttaagt	960
ttgaccttag atcactggaa agatgtcgag cggctcgtc acaaccagtc gtagatgtc	1020
aagaagagac gttgggttac cttctgtctt gcagaatggc caacctttaa cgtcggatgg	1080
ccgcgagacg gcacctttaa ccgagacctc atcaccagg ttaagatcaa ggtctttca	1140
cctggcccgc atggacaccc agaccagtc cctacatcg tgacctggga agccttggt	1200
tttgaccccc ctccctgggt caagcccttt gtacacccta agcctccgc tcctcttctt	1260
ccatccgcgc cgtctctccc ccttgaacct cctctttcga ccccgctca atcctccctt	1320
tatccagccc tcactccttc tctaggcgcc ggccggatcc cagtgtgtg gtacgtagga	1380
attcgcagc acagtgtcg acctgtggaa tgtgtgtcag ttaggggtg gaaagtcccc	1440
aggctcccca gcaggcagaa gtatgcaaag catgcatctc aattagtcag caaccagtg	1500
tggaaagtcc ccaggctccc cagcaggcag aagtatgcaa agcatgcac tcaattagtc	1560
agcaaccata gtcccgcccc taactccgc catcccgccc ctaactccgc ccagttccgc	1620
ccattctccg ccccatggct gactaatttt tttattttat gcagaggccg aggcgcctc	1680
ggcctctgag ctattccaga agtagtgagg aggtttttt ggaggcctag gcttttcaa	1740
acgtgcttg aggtgaagg tgcgttgctg gcgtttttcc ataggctccg ccccccgtac	1800
gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg actataaaga	1860
taccaggcgt ttccccctgg aagctccctc gtgcgtctc ctgttcgcac cctgccgctt	1920
accggatacc tgtccgcctt tctcccttcg ggaagcgagg cgctttctca tagctcacgc	1980
tgtaggatc tcagttcgggt gtaggtcgtt cgctccaagc tgggctgtgt gcacgaaccc	2040

cccgttcagc cgcaccgctg cgccttatcc ggtaactatc gtcttgagtc caacccggta 2100
 agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag agcgaggat 2160
 gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac tagaaggaca 2220
 gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt tggtagctct 2280
 tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa gcagcagatt 2340
 acgatcgata aaataaaaga ttttatitag tctccagaaa aaggggggaa tgaaagaccc 2400
 cacctgtagg ttggcaagc tagcttaagt aacgccattt tgcaaggcat ggaaaaatac 2460
 ataactgaga atagagaagt tcagatcaag gtcaggaaca gatggaacag ctgaatatgg 2520
 gccaaacagg atatctgtgg taagcagttc ctgccccggc tcaggggcaa gaacagatgg 2580
 aacagctgaa tatgggcaa acaggatatc tgtgtaagc agttcctgcc ccggctcagg 2640
 gccagaaca gatggtcccc agatcggtc cagccctcag cagtttctag agaaccatca 2700
 gatgtttcca gggtgcccca aggacctgaa atgacctgt gccttatttg aactaaccaa 2760
 tcagttcgt tctcgcttct gtgcgcgc tctgtctccc cgagctcaat aaaagagccc 2820
 acaaccctc actcggggcg ccagtcctcc gattgactga gtcgccggg taccctgta 2880
 tccaataaac cctcttgtag ttgatccga cttgtggtct cgctgttctt tgggagggtc 2940
 tcctctgagt gatigactac ccgtcagcgg gggcttttca catgcagcat giatcaaat 3000
 taatttggtt tttttctta agtatttaca ttaaatggcc atagttgcat taatgaatcg 3060
 gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg 3120
 actcgtcgc ctcggtcgtt cggctcggc gagcggatc agctcactca aaggcggtaa 3180
 tacggttata cacagaatca ggggataacg caggaaagaa catgtgagca aaaggccagc 3240
 aaaaggccag gaaccgtaaa aaggccgct tgcctggcgtt ttccatagg ctccgcccc 3300
 ctgacgagca tcacaaaaat cgacgtcaa gtcagagggt gcgaaaccg acaggactat 3360
 aaagatacca ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt ccgacctgc 3420
 cgcttaccgg atacctgtcc gcctttctcc cttcgggaag cgtggcgctt tctcatagct 3480

cacgctgtag gtatctcagt tcgggtgtagg tcgttcgctc caagctgggc tgtgtgcacg 3540
 aaccccccggt tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc 3600
 cggtaaagaca cgacttatcg ccactggcag cagccactgg taacaggatt agcagagcga 3660
 ggtatgtagg cggtgctaca gagttcttga agtgggtggc taactacggc tacactagaa 3720
 ggacagtatt tggatatctgc gctctgctga agccagttac cttcggaaaa agagttggta 3780
 gctcttgatc cggcaaacaa accaccgctg gtagcgggtg tttttttgtt tgcaagcagc 3840
 agattacgcg cagaaaaaaaa ggatctcaag aagatccttt gatcttttct acgggggtctg 3900
 acgctcagtg gaacgaaaac tcacgttaag ggatttttgt catgagatta tcaaaaagga 3960
 tcttcaccta gatccttita aattaaaaat gaagtttgcg gccgcaaacc aatctaaagt 4020
 atatatgagt aaacttggtc tgacagttac caatgcttaa tcagtggaggc acctatctca 4080
 gcgatctgtc tatttcgttc atccatagtt gcctgactcc ccgtcgtgta gataactacg 4140
 atacgggagg gcttaccatc tggccccagt gctgcaatga taccgcgaga cccacgctca 4200
 ccggctccag atttatcagc aataaaccag ccagccggaa gggccgagcg cagaagtgg 4260
 cctgcaactt tatccgcctc catccagctc attaatgtt gccgggaagc tagagtaagt 4320
 agttcgccag ttaatagttt gcgcaacgtt gttgccattg ctacaggcat cgtgggttca 4380
 cgctcgtcgt ttggtatggc ttcatcagc tccggttccc aacgatcaag gcgagttaca 4440
 tgatccccc tgttgtgcaa aaaagcgggt agtccttcg gtccctccgat cgttgtcaga 4500
 agtaagttgg ccgcagtgtt atcaactatg gttatggcag cactgcataa ttctcttact 4560
 gtcatgccat ccgtaagatg cttttctgtg actggtgagt actcaaccaa gtcattctga 4620
 gaatagtgtg tgcggcgacc gagttgctct tgcccggcgt caacacggga taataccgcg 4680
 ccacatagca gaactttaaa agtgctcatc attggaaaac gttcttcggg gcgaaaactc 4740
 tcaaggatct taccgctgtt gagatccagt tcgatgtaac ccactcgtgc acccaactga 4800
 tcttcagcat cttttacttt caccagcgtt tctgggtgag caaaaacagg aaggcaaaat 4860
 gccgcaaaaa agggaataag ggcgacacgg aaatgttgaa tactcatact cttccttttt 4920

caatattatt gaagcattta tcagggttat tgtctcatga gcggatacat atttgaatgt 4980

atttagaaaa ataaacaaat aggggttcgc cgcacatttc 5020

<210> 8

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> A sense strand for CREx2hb

<400> 8

cccaagcttg atatcgaatt cgacgtcaca gtatgacggc catgggaatt cgacgtcaca 60

gtatgacggc catggggatc ccg 83

<210> 9

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> An antisense strand for CREx2hb

<400> 9

cgggatcccc atggccgtca tactgtgacg tcgaattccc atggccgtca tactgtgacg 60

tcgaattcga tatcaagctt ggg 83

<210> 10

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> A sense strand for CREx2bp

<400> 10

tgcactgcag gaattcccat ggccgtcata ctgtgacgtc gaattcccat ggccgtcata 60

ctgtgacgtc ggatcccg 78

<210> 11
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An antisense strand for CREx2bp

<400> 11
 cgggatccga cgtcacagta tgacggccat gggaattcga cgtcacagta tgacggccat 60
 gggaattcct gcagtgcg 78

<210> 12
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> A sense primer

<400> 12
 tcgactgcag cccatggccg tcatactgtg 30

<210> 13
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An antisense primer

<400> 13
 tgcaactgcag gtcggagctg actgttctgg 30

<210> 14
 <211> 264
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Vasoactive intestinal peptide promoter

<400> 14
 tcgactgcag cccatggccg tcatactgtg tgacgtcttt cagagcactt tgtgattgct 60

cagtcctaag tataagccct ataaaatgat gggctttgaa atgctggta gggtagagt	120
agaagcacca gcaggcagta acagccaacc ctagccatt gctaaggga gagaactgt	180
ggagccttc tottactccc aggacticag cacctaagac agctccaaa caaaccagaa	240
cagtcagctc cgacctgcag tgca	264